# SEQUENCE LISTING

<110>    Seoul National University Industry Foundation

<120>    ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
         AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT

<130>    20020-02USA

<140>    US 10/660,499
<141>    2003-09-12

<150>    KR 2003-19069
<151>    2003-03-27

<160>    9

<170>    KopatentIn 1.71

<210>    1
<211>    1089
<212>    DNA
<213>    Glycine max

<220>
<221>    CDS
<222>    (52)..(816)
<223>    Glycine max expansin (GmEXP1)


<400>    1
gcacgagctt caacctctca tcattaggca ttcagcaagc aagaaaaaaa a                51

atg  ggc aaa atc atg  ctt  gtt  ttg ggt  agc ctc att  gga tta  tgc tgt    99
Met Gly Lys Ile Met  Leu Val Leu Gly Ser Leu Ile  Gly Leu Cys Cys
 1               5                    10                   15
ttc  aca atc act acc  tat gcc  ttc  tca cct tct  gga tgg acc  aac gcc     147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
             20                   25                   30
cat  gcc act ttt  tat  ggg ggt  agt gat  gct tca  gga act atg  ggg gga   195
His  Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser  Gly Thr Met Gly Gly
          35                   40                   45
gct tgt ggg  tat  ggg aat ctg  tat  gca act ggg tat  gga act aga act     243
Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
    50                   55                   60
gca gct tta  agc act  gcc tta  ttt  aat  gat gga gct tcc  tgt ggt cag     291
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
65                   70                   75                   80
tgc  tac aaa att ata tgt  gat  tac aaa tca  gac tct  aga tgg  tgc atc     339
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile

```
aaa gga aga tct  gta acc gta  act gcc aca aac  ttt tgc cct  ccc aat   387
Lys Gly Arg Ser  Val Thr Val  Thr Ala Thr Asn  Phe Cys Pro  Pro Asn
           100              105              110
ttc  gcc ctt  cct  aac aac aat  gga ggc tgg tgc aac  cca cca ctc  aag 435
Phe  Ala Leu  Pro  Asn Asn Asn  Gly Gly Trp Cys Asn  Pro Pro Leu  Lys
        115              120              125
cat ttt  gat  atg gcc caa ccc  gct tgg gaa aag att  ggt att tac aga    483
His Phe  Asp  Met Ala Gln Pro  Ala Trp Glu Lys Ile  Gly Ile Tyr Arg
   130              135              140
gga ggg atc gtc  ccc gtg cta  ttt caa  agg gtt cca tgc  aaa aag cat    531
Gly Gly Ile Val  Pro Val Leu  Phe Gln  Arg Val Pro Cys  Lys Lys His
145              150              155              160
gga ggg gtt agg  ttc agt  gtg aat ggg agg gac  tac ttt  gag cta  gta   579
Gly Gly Val Arg  Phe Ser  Val Asn Gly Arg Asp  Tyr Phe  Glu Leu  Val
                 165              170              175
ttg atc agc aat  gtg ggg ggt gct gga tcc atc caa tca gtg  ttc att      627
Leu Ile Ser Asn  Val Gly Gly Ala Gly Ser Ile Gln Ser Val  Phe Ile
           180              185              190
aaa ggc tca aaa  act gga tgg atg  gca atg  tca aga aat  tgg ggt tct    675
Lys Gly Ser Lys  Thr Gly Trp Met  Ala Met  Ser Arg Asn  Trp Gly Ser
        195              200              205
aat  tgg caa tcc  aat gcg tat  ttg  aat  ggt caa tct  ttg  tcc ttc  agg 723
Asn  Trp Gln Ser  Asn Ala Tyr  Leu  Asn  Gly Gln Ser  Leu  Ser Phe  Arg
   210              215              220
gtc acc  acc act  gat gga gag acc aga gtt  ttc  caa gat att gtt cca    771
Val Thr  Thr Thr  Asp Gly Glu Thr Arg Val  Phe  Gln Asp Ile Val Pro
225              230              235              240
gta agt  tgg aca ttc  ggc caa act  ttc  tct agc cca  gtt cag ttc  taag 820
Val Ser  Trp Thr Phe  Gly Gln Thr  Phe  Ser Ser Pro  Val Gln Phe
                 245              250              255
ctgattacag ataaaccaac caacggctga ggcgtgcttt tttattttat tactggagct       880
gcccgccacc cttcttctgg ttttgattat tcccatcaac tccaagccct ctatcaaggc       940
ataaattctt atcaataata caatcaatca ccatcatatc atcataagct tgtatatcaa      1000
ataaacatct ttcaagttta aattaattta tactataaat tgttgtaata tcattatagt      1060
tgaagttcaa aaaaaaaaaa aaaaaaaaa                                        1089
```

<210> 2
<211> 255
<212> PRT
<213> Glycine max

<400> 2
```
Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys
 1               5                   10                  15
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
            20                  25                  30
His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
        35                  40                  45
```

Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
      50              55              60
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
  65              70              75              80
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile
              85              90              95
Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
              100             105             110
Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
          115             120             125
His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
      130             135             140
Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
145             150             155             160
Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
              165             170             175
Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
          180             185             190
Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
          195             200             205
Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
      210             215             220
Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
225             230             235             240
Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
              245             250             255


<210>    3
<211>    44
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Primer


<400>    3
nnggatccga ygcntcnggn acnatgggyg gygctgygyt angg                    44


<210>    4
<211>    37
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Primer

3

<400> 4
nnggatcctt kswytgccar ttnnsnccc arttnck                          37


<210> 5
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe


<400> 5
gaygcnwsng gnacnatggg nggngcntgy ggntayggna ayytntaygc nacnggntay   60
ggnacnmgna cngcngcnyt nwsnacngcn ytnttyaayg ayggngcnws ntgyggncar  120
tgytayaara thathtgyga ytayaarwsn gaywsnmgnt ggtgyathaa rggnmgnwsn  180
gtnacngtna cngcnacnaa yttytgyccn ccnaayttyg cnytnccnaa yaayaayggn  240
ggntggtgya ayccnccnyt naarcaytty gayatggcnc arccngcntg ggaraarath  300
ggnathtaym gnggnggnat hgtnccngtn ytnttycarm gngtnccntg yaaraarcay  360
ggnggngtnm gnttywsngt naayggnmgn gaytayttyg arytngtnyt nathwsnaay  420
gtnggnggng cnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac nggntggatg  480
gcnatgwsnm gnaaytgggg nwsnaaytgg carwsnaay                        519


<210> 6
<211> 269
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA probe (antisense)


<400> 6
aauaaaauaa aaaagcacgc cucagccguu gguugguuua ucuguaauca gcuuagaacu   60
gaacugggcu agagaaaguu uggccgaaug uccaacuuac uggaacaaua ucuuggaaaa  120
cucuggucuc uccaucagug guggugaccc ugaaggacaa agauugacca uucaaauacg  180
cauuggauug ccaauuagaa ccccaauuuc uugacauugc cauccaucca guuuuugagc  240
cuuuaaugaa cacugauugg auggaucca                                   269


<210> 7
<211> 389
<212> RNA
<213> Artificial Sequence

<220>
<223> RNA probe (sense)

<400>    7
uggauccauc caaucagugu ucauuaaagg cucaaaaacu ggauggaugg caaugucaag  60
aaauuggggu ucuaauuggc aauccaaugc guauuugaau ggucaaucuu uguccuucag 120
ggucaccacc acugauggag agaccagagu uuuccaagau auuguuccag uaaguuggac 180
auucggccaa acuuucucua gcccaguuca guucuaagcu gauuacagau aaaccaacca 240
acggcugagg cgugcuuuuu uauuuuauua cuggagcugc ccgccacccu ucuucugguu300
uugauuauuc ccaucaacuc caagcccucu aucaaggcau aaauucuuau caauaauaca 360
aucaaucacc aucauaucau cauaagcuu                                  389

<210>    8
<211>    28
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Primer

<400>    8
accaagcttc aacctctcat cattaggc                                    28

<210>    9
<211>    29
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    Primer

<400>    9
accaagcttg gagttgatgg gaataatca                                   29